



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 190621

TO: Sean McGarry
Location: REM-2C18
Art Unit: 1635
Thursday, May 2006
Case Serial Number: 10/714796

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner McGarry,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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190621

STIC-Biotech/ChemLib

From: McGarry, Sean
Sent: Friday, May 19, 2006 1:06 PM
To: STIC-Biotech/ChemLib
Subject: SEQ SEARCH 10/714,796

Sean McGarry 73484
AU 1635
571.272.0761
REM 2C18 Mailbox
PHP
10/714,796

Please, a length limited search of SEQ ID NO: 122 (nt \leq 75).

Thank You.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact:***

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.

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Wed May 24 10:03:07 2006

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 10:56:45 ; Search time 2444 Seconds
(without alignments)
523.301 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtggaattaccagcca 20

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2571824

Minimum DB seq length: 0
Maximum DB seq length: 75Post-processing: Minimum Match 0%
Maximum Match 100%
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15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	50	2	AR682287 Sequence
2	14.2	71.0	68	2	AR356566 Sequence
3	14.2	71.0	68	2	AR38122 Sequence
4	13.6	68.0	29	2	AR044889 Sequence
5	13.6	68.0	29	2	AR096454 Sequence
6	13.6	68.0	29	2	174371 Sequence 34
7	13.6	68.0	45	2	155019 Sequence 43
8	13.6	68.0	50	2	AX960383 Sequence
9	13.6	68.0	51	2	CQ007345 Sequence
10	13.2	66.0	22	2	BD177702 Process f
11	13.2	66.0	22	2	CQ830789 Sequence
12	13.2	66.0	22	2	AX503513 Sequence
13	13.2	66.0	41	2	AX574446 Sequence
14	13.2	66.0	44	2	BD177703 Process f
15	13.2	66.0	44	2	CQ830790 Sequence
16	13.2	66.0	44	2	AX503514 Sequence
17	13.2	66.0	65	2	AX484110 Sequence
18	13	65.0	60	2	BD006973 Artificialia

19	12.8	64.0	20	2	AR241114 Sequence
20	12.8	64.0	21	2	AR072146 Sequence
21	12.8	64.0	24	2	AR429847 Sequence
22	12.8	64.0	24	2	AX042025 Sequence
23	12.8	64.0	56	2	CS191956 Sequence
24	12.8	64.0	59	2	BD006952 Artificialia
25	12.8	64.0	65	2	CQ559344 Sequence
26	12.8	64.0	69	11	AY538960 Champso
27	12.6	63.0	20	2	BD016897 Rice-orig
28	12.6	63.0	20	2	DD176246 Verificat
29	12.6	63.0	20	2	AX803985 Sequence
30	12.6	63.0	24	2	CS027277 Sequence
31	12.6	63.0	24	2	CS027278 Sequence
32	12.6	63.0	31	2	BD016889 Rice-orig
33	12.6	63.0	42	2	AR071190 Sequence
34	12.6	63.0	51	5	AY082067 Homo Bapi
35	12.6	63.0	59	2	CS052969 Sequence
36	12.6	63.0	59	2	CS183920 Sequence
37	12.6	63.0	59	2	AX600107 Sequence
38	12.6	63.0	60	2	CQ541589 Sequence
39	12.6	63.0	65	2	CQ560799 Sequence
40	12.6	63.0	65	2	AX483910 Sequence
41	12.4	62.0	17	2	AX532402 Sequence
42	12.4	62.0	17	2	AX532403 Sequence
43	12.4	62.0	17	2	AX532404 Sequence
44	12.4	62.0	17	2	AX532405 Sequence
45	12.4	62.0	25	2	AX534464 Sequence

ALIGNMENTS

RESULT 1	AR682287	Sequence 1716 from patent US 6905827.	50 bp	DNA	linear	PAT 12-SBP-2005
LOCUS	AR682287	Sequence 1716 from patent US 6905827.				
DEFINITION	AR682287					
ACCESSION	AR682287					
VERSION	AR682287.1	GI:74464057				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 50)					
AUTHORS	Wohlgenuth,J., Fry,K., Woodward,R. and Ly,N.					
TITLE	Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases					
JOURNAL	Patent: US 6905827-A 1716 14-JUN-2005;					
FEATURES	Expression Diagnostics, Inc.; So. San Francisco, CA					
source	Location/Qualifiers					
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ORIGIN	/organism="unknown"					
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Db	19 ACGTGAATTATATCAGAC 37					
RESULT 2	AR356566	68 bp	DNA	linear	PAT 17-AUG-2003	
LOCUS	AR356566					
DEFINITION	Sequence 2684 from patent US 6593114.					
ACCESSION	AR356566					
VERSION	AR356566.1	GI:33762650				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
	Unclassified.					

REFERENCE 1 (bases 1 to 68)
AUTHORS Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and

TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 2684 15-VUL-2003;
Human Genome Sciences, Inc.; Rockville, MD

FEATURES
source 1..68
Location/Qualifiers

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Db 35 CATGAATTATCCGACCA 53

RESULT 3
LOCUS AR538122 68 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2684 from patent US 6737248.
ACCESSION AR538122
VERSION AR538122.1 GI:53929339

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 68)
AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6737248-A 2684 18-MAY-2004;
Human Genome Sciences, Inc.; Rockville, MD

FEATURES
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Location/Qualifiers

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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGTGAATTATACGACCA 20
Db 35 CATGAATTATCCGACCA 53

RESULT 4
LOCUS AR044889 29 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 43 from patent US 5817759.
ACCESSION AR044889
VERSION AR044889.1 GI:5966354

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 29)
AUTHORS Margolske,R.F.
TITLE Gustducin polypeptides and fragments
JOURNAL Patent: US 5817759-A 43 06-OCT-1998;
Location/Qualifiers

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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATACGACCA 20
Db 9 ACGTTTAAATTATTCAGCCA 28

RESULT 5
LOCUS AR096454 29 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 43 from patent US 6008000.
ACCESSION AR096454
VERSION AR096454.1 GI:10025269

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 29)
AUTHORS Margolske,R.F.
TITLE Gustducin materials and methods
JOURNAL Patent: US 6008000-A 43 28-DEC-1999;
Location/Qualifiers

FEATURES
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ORIGIN

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Db 9 ACGTTTAAATTATTCAGCCA 28

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DEFINITION Sequence 34 from patent US 5688662.
ACCESSION I74371
VERSION I74371.1 GI:3010512

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 29)
AUTHORS Margolske,R.F.
TITLE Gustducin polynucleotides, vectors, host cells and recombinant
methods
JOURNAL Patent: US 5688662-A 34 18-NOV-1997;
Location/Qualifiers

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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATACGACCA 20
Db 9 ACGTTTAAATTATTCAGCCA 28

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LOCUS I55019 45 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 43 from patent US 5646156.
ACCESSION I55019
VERSION I55019.1 GI:2476222

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 45)
TITLE Jacobson,M.A., Johnson,R.G. and Salvatore,C.A.
JOURNAL Inhibition of eosinophil activation through A3 adenosine receptor
FEATURES Patent: US 5646156-A 43 08-JUL-1997;
source Location/Qualifiers
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Qy 1 ACGTGAATTATACCGCA 20
Db 32 ACCGAGATGACACCGCA 13
RESULT 8
LOCUS AX960383 50 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 59 from Patent WO03102192.
ACCESSION AX960383
VERSION AX960383.1 GI:40880510
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1 Cosme,J., Ward,A., Villard,L., Williams,P. and Hamilton,B.
TITLE Methods of purification of cytochrome p450 proteins and of their
JOURNAL crystallizing
Patent: WO 03102192-A 59 11-DEC-2003;
Astex Technology Limited (GB)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ACGTGAATTATACCGCA 20
Db 16 ACGGAGACTTATACCGCA 35
RESULT 9
LOCUS CQ007345 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 5985 from Patent WO0147944.
ACCESSION CQ007345
VERSION CQ007345.1 GI:41013986
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1 Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof
JOURNAL Patent: WO 0147944-A 5985 05-JUL-2001;
Curegen Corporation (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/note="Accession number cg43960450"
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ACGTGAATTATACCGCA 20
Db 13 ACGTCAATTATACCGCA 32
RESULT 10
LOCUS BD177702/c 22 bp DNA linear PAT 16-APR-2003
DEFINITION Process for producing L-glutamine by fermentation and
L-glutamine-producing microorganism.
ACCESSION BD177702
VERSION BD177702.1 GI:30014964
KEYWORDS JP 2002300887-A/14.
SOURCE JP 2002300887-A/14.
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1 (bases 1 to 22)
Kurashiki,O., Moriyuchi,K., Izui,H., Kawashima,N., Nakamatsu,T. and
TITLE Process for producing L-glutamine by fermentation and
JOURNAL L-glutamine-producing microorganism
Patent: JP 2002300887-A 14 15-OCT-2002;
AJINOMOTO CO INC
COMMENT
OS Artificial Sequence
OS Unknown
PN JP 2002300887-A/14
PD 15-OCT-2002
PI 30-MAY-2001 JP 2001162806
PI JUN NAKAMURA,KAYO MORIUCHI,HIROSHI IZUI,NOBUKI KAWASHIMA, PI
TSUYOSHI NAKAMATSU OSAWU KURASHIKI
PC C12N1/21,C12N1/13,C12N9/12,C12P13/14,C12N1/21,C12R1/15, PC
C12N1/21,C12R1/15,C12N9/12,C12P13/14,C12R1/13, PC
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Qy 1 ACGTGAATTATACCGC 18
Db 19 ACGTCAATTATACGAC 2
RESULT 11
LOCUS CQ830789/c 22 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 16 from Patent EP1424398.
ACCESSION CQ830789

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VERSION      CQ830789.1 GI:50251068
KEYWORDS
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 Nakamura,J., Izui,H., Moriyuchi,K., Kawashima,H., Nakamatsu,T. and
AUTHORS      Kurahashi,O.
TITLE        Method for producing L-glutamine by fermentation and L-glutamine
              producing bacterium
JOURNAL      Patent: EP 1424398-A 16 02-JUN-2004;
              Ajinomoto Co., Inc. (JP)
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Best Local Similarity 83.3%; Pred. No. 1.9e+05;
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Qy
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AX503513/c      22 bp   DNA   linear   PAT 27-SEP-2002
LOCUS           Sequence 16 from Patent EP1229121.
DEFINITION      AX503513
ACCESSION       AX503513
VERSION         AX503513.1 GI:23385805
KEYWORDS
SOURCE         synthetic construct
ORGANISM       synthetic construct
OTHER SEQUENCES; artificial sequences.
REFERENCE
  AUTHORS      1 Nakamura,J., Izui,H., Moriyuchi,K., Kawashima,H., Nakamatsu,T. and
              Kurahashi,O.
  TITLE        Method for producing L-glutamine by fermentation and L-glutamine
              producing bacterium
  JOURNAL      Patent: EP 1229121-A 16 07-AUG-2002;
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Qy
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19 ACGTTCATTATACGAGC 2

RESULT 13
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LOCUS           AX574446 41 bp   DNA   linear   PAT 07-JAN-2003
DEFINITION      Sequence 18 from Patent WO02068629.
ACCESSION       AX574446
VERSION         AX574446.1 GI:27551770
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
AUTHORS        1 Pachuk,C.J. and McCallus,D.E.
TITLE          Dna constructs for cytoplasmic and mitochondrial expression and
              methods of making and using same
JOURNAL        Patent: WO 02068629-A 18 06-SEP-2002;
              Wyeth (US)
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Qy
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Db
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LOCUS           Process for producing L-glutamine by fermentation and
DEFINITION      L-glutamine-producing microorganism.
ACCESSION       BD177703
VERSION         BD177703.1 GI:30014965
KEYWORDS
SOURCE         synthetic construct
ORGANISM       synthetic construct
OTHER SEQUENCES; artificial sequences.
REFERENCE
  AUTHORS      1 (bases 1 to 44)
              Nakamura,J., Moriyuchi,K., Izui,H., Kawashima,H., Nakamatsu,T. and
              Kurahashi,O.
  TITLE        Process for producing L-glutamine by fermentation and
              L-glutamine-producing microorganism
  JOURNAL      Patent: JP 2002300887-A 15 15-OCT-2002;
              AJINOMOTO CO. INC
  COMMENT      OS Artificial Sequence
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              PN JP 2002300887-A/15
              PD 15-OCT-2002
              PF 30-MAY-2001 JP 2001162806
              PI JUN NAKAMURA,KAYO MORIYUCHI,HIROSHI IZUI,NOBUKI KAWASHIMA,PI
              TSUYOSHI NAKAMATSU,OSAMU KURAHASHI
              PC C12N15/09,C12N1/21,C12P13/14/(C12N1/21,C12R1:15),PC
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Qy
1 ACGTGAATTATACGAGC 18
19 ACGTTCATTATACGAGC 24

Db
41 ACGTTCATTATACGAGC 24

RESULT 15

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CO830790/c . CO830790 44 bp DNA linear PAT 12-JUL-2004
LOCUS Sequence 17 from Patent EP1424398.
DEFINITION CO830790
ACCESSION CO830790
VERSION CO830790.1 GI:50251069
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Nakamura,T., Izui,H., Moriguchi,K., Kawashima,H., Nakamatsu,T. and
Kurahashi,O.
TITLE Method for producing L-glutamine by fermentation and L-glutamine
JOURNAL producing bacterium
Patent: EP 1424398-A 17 02-JUN-2004;
Ajinomoto Co., Inc. (JP)
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Best Local Similarity 83.3%; Pred. No. 2e+05;
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Job time : 246 secs

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GenCore version 5.1.8
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Run on: May 23, 2006, 10:37:30 ; Search time 290 Seconds
(without alignments)
480.845 Million cell updates/sec

Sequence: 1 acgttggaattataccagcca 20

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 75
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	13	ADR73258	Adi73358 Anti-sense
2	15.2	76.0	40	10	ADD24544	Adi74544 DNA poly
3	14.8	74.0	32	3	ABK12019	Abk12019 Human cyc
4	14.2	71.0	50	6	ABZ01725	Abz01725 Human leu
5	14.2	71.0	68	2	AAV76995	AAv76995 Staphyloc
6	14.2	71.0	75	10	ACD93498	AcD93498 Human co
7	13.8	69.0	25	9	ACI58064	ACi58064 Human mic
8	13.8	69.0	25	9	ACI58693	ACi58693 Human mic
9	13.8	69.0	25	9	ACI58692	ACi58692 Human mic
10	13.6	68.0	29	2	AAQ51108	AAq51108 Alpha sub
11	13.6	68.0	29	2	AAV54426	AAv54426 Nucleoid
12	13.6	68.0	29	3	AAZ49047	AAz49047 PCR prime
13	13.6	68.0	29	8	ABT15720	ABt15720 Human can
14	13.6	68.0	29	9	ACA62089	ACa62089 G protein
15	13.6	68.0	30	12	ADP09053	ADp09053 PCR prime
16	13.6	68.0	30	14	ADY02430	ADy02430 PCR prime
17	13.6	68.0	45	2	AAU70608	AAu70608 RT-PCR pr
18	13.6	68.0	45	2	AAU06766	AAu06766 primer 25

19	13.6	68.0	50	12	ADJ87572	Adj87572 Human cye
20	13.6	68.0	51	4	AA132777	AA132777 Human SNP
21	13.2	66.0	22	6	AB082104	Abg82104 Brevibact
22	13.2	66.0	22	12	AD080107	Ado80107 Gutamate
23	13.2	66.0	26	2	AA787460	AA787460 Chicken/h
24	13.2	66.0	40	6	ABK96453	Abk96453 PCR prime
25	13.2	66.0	41	6	ADH13895	Adh13895 Human max
26	13.2	66.0	44	6	ABK96460	Abk96460 PCR prime
27	13.2	66.0	44	6	AB082105	Abg82105 Brevibact
28	13.2	66.0	44	12	AD080108	Ado80108 Gutamate
29	13.2	66.0	65	6	ABE27463	Abz27463 Candida e
30	13	65.0	60	2	AAV23314	AAV23314 Lactococc
31	13	65.0	60	15	ABE86265	Aee86265 WML3 prob
32	12.8	64.0	20	10	ABX78268	Abx78268 Human biff
33	12.8	64.0	21	2	AAx76378	Aax76378 Zee may's
34	12.8	64.0	21	6	ADD42928	Ad42928 Maize sug
35	12.8	64.0	21	14	AEC74822	Aec74822 Maize spec
36	12.8	64.0	29	3	AAC66328	Aac66328 DSPS spec
37	12.8	64.0	29	3	AAA04617	Aaa04617 Polymorph
38	12.8	64.0	40	15	ABF10355	Aef10355 B19 virus
39	12.8	64.0	40	15	AEF10354	Aef10354 B19 virus
40	12.8	64.0	41	4	AAH75822	Aah75822 Human g p
41	12.8	64.0	59	14	AED81864	Aed81864 Hyperimmu
42	12.8	64.0	59	2	AAV23193	Aav23193 Lactococc
43	12.8	64.0	60	6	ABK98622	Abk98622 Lambda CP
44	12.8	64.0	60	9	ACD13873	Adc13873 L. lactis
45	12.8	64.0	60	14	ADZ62209	Adz62209 Mwine chr

ALIGNMENTS

ID	ADR72358	standard; DNA; 20 BP.
XX	ADR72358	
AC	ADR72358;	
DT	02-DEC-2004	(first entry)
DE	Anticentase oligo targeted to human kinesin-like 1, ISIS 344894.	
XX		
KW	Anticentase; kinesin-like 1; N2 kinesin; binc kinesin;	
KW	cellular proliferation; cancer; B-cell leukaemia; autoimmune disease;	
KW	carpal tunnel syndrome; Raynaud's phenomenon; systemic sclerosis;	
KW	Storgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis;	
KW	systemic lupus erythematosus; human; ss; ISIS 344894; rat.	
XX		
OS	Homo sapiens.	
OS	Rattus sp.	
OS	Synthetic.	
XX		
Key	modified_base	Location/Qualifiers
FT	1..20	
FT	/*tag= a	
FT	/mod_base= OTHER	
FT	/note= "OTHER= phosphorothioate nucleotide. All cytosines	
FT	are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are	
FT	2'-methoxyethyl nucleotides."	
PN	US2004180847-A1.	
XX		
PD	16-SEP-2004.	
XX		
PF	17-NOV-2003; 2003US-00714796.	
XX		
PR	23-MAY-2002; 2002US-00156603.	
XX		
PA	(DOB1/) DOBIE K W.	
PA	(KOLL/) KOLLER E.	
XX		
XX	Dobie KW, Koller E;	
PI		
XX		

DR WPI; 2004-652550/63.

XX New antisense compound 8 to 80 nucleobases in length targeted to a
PT nucleic acid molecule encoding kinesin-like 1, useful for treating an
PT animal having a disease or condition such as cancer, tumor, autoimmune
XX disease.

XX Claim 35; SEQ ID NO 122; 110pp; English.

XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of kinesin-like 1. The superfamily
CC of kinesins function as molecular engines to bind and transport vesicles
CC and organelles along microtubules using energy supplied by ATP. Kinesin-
CC like 1, a member of the N2 (also called bimc) family of kinesins, is
CC involved in separating the chromosomes by directing their movement along
CC microtubules in the bipolar spindle. Kinesin-like 1 is also known as
CC KNSL1, Eg5, Heeg5, HKSP, KIF11, thyroid interacting protein 5 and TRIP5.
CC Inhibition of kinesin-like 1 may be a target for arresting cellular
CC proliferation in cancer, due to its central role in mitosis. Expression
CC of kinesin-like 1 expression may contribute to other disease states such
CC as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome,
CC Raynaud's phenomenon, systemic sclerosis, Sjogren's syndrome, rheumatoid
CC arthritis, polymyositis and polyarteritis. Kinesin-like 1 is an
CC autoantigen identified in systemic lupus erythematosus. The invention
CC relates to antisense nucleic acid oligomers, targeted to the gene
CC encoding kinesin-like 1. Also provided are methods of screening for
CC modulators of kinesin-like 1 and to methods of modulating the expression
CC of kinesin-like 1. At least a portion of the compound hybridises with RNA
CC to form an oligonucleotide-RNA duplex. It has at least one modified
CC internucleoside linkage, sugar moiety, or nucleobase. It has at least one
CC 2'-O-methoxyethyl sugar moiety, phosphorothioate internucleoside linkage,
CC or one cytosine which is a 5-methylcytosine. The antisense compound may
CC comprise an antisense nucleic acid molecule that is specifically
CC hybridisable with a 5'-untranslated region (UTR), with a start region,
CC with a coding region, with a 3'-UTR, with an intron, or with an intron-
CC exon junction of a nucleic acid molecule encoding kinesin-like 1.
CC Oligonucleotides were synthesised via solid phase P(III) phosphoramidite
CC chemistry. The present sequence is an antisense oligo targeted to human
CC kinesin-like 1, ISIS #344894.

XX SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 13; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACCA 20
DB 1 ACGTGAATTATACGACCA 20

XX RESULT 2
XX ADD24544/c
XX ID ADD24544 standard; DNA; 40 BP.
XX AC ADD24544;
XX DT 15-JAN-2004 (first entry)
XX DE DNA polymerase III subunit protein related PCR primer, SEQ ID No 63.
XX KW DNA polymerase III replicase; dnaB; hola; holB; holC; holD; holE; dnaX;
XX dnaN; ssB; dnaQ; bacterial DNA replication; bacterial infection;
XX PCR; primer; ss.
XX OS Unidentified.
XX PN WO200292769-A2.
XX PP 21-NOV-2002.
XX PF 14-MAY-2002; 2002WO-US015111.
XX DR

PR 14-MAY-2001; 2001US-0290725P.
PR 05-NOV-2001; 2001US-0332644P.
XX (REPL-) REPLIDYNE INC.
XX PA Bullard JM, Janjic N, Mchenry CS;
XX WPI; 2003-120672/11.

XX Screening for a compound that modulates the activity of γ . pests and/or
PT P. aeruginosa DNA polymerase III replicase, useful for reducing bacterial
PT DNA replication and infection in animals, plants, humans and surrounding
XX environment.

XX Example 38; SEQ ID NO 63; 388pp; English.

XX The invention relates to a novel screening method for a compound that
CC modulates the activity of a DNA polymerase III replicase. The novel
CC method comprises contacting an isolated replicase with at least one test
CC compound under conditions permissive for replicase activity, and
CC comparing the activity of the replicase in the presence and absence of
CC the test compound, where a change in the activity of the replicase
CC indicates a compound that modulates the activity of the replicase. The
CC replicase comprises an isolated nucleic acid from *Yersinia pestis* or a
CC *Pseudomonas aeruginosa* encoding a DNA polymerase III subunit protein. The
CC DNA polymerase III subunit proteins include dnaB, hola, holB, holC, holD,
CC hola, dnaX, dnaN, ssB, dnaQ, and dnaQ. The methods and compositions of
CC the present invention are useful for reconstituting replicases and
CC polymerases for sequencing, amplification and screening for compounds
CC which modulate the function of the polymerase or replicase particularly
CC in bacterial DNA replication, thereby reducing bacterial infection in
CC animals, plants, humans and the surrounding environment. This
CC polynucleotide sequence represents a PCR primer relating to the DNA
CC polymerase III subunit proteins of the invention.

XX SQ Sequence 40 BP; 8 A; 9 C; 9 G; 14 T; 0 U; 0 Other;

XX Query Match 76.0%; Score 15.2; DB 10; Length 40;
XX Best Local Similarity 85.0%; Pred. No. 7.3e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGACCA 20
DB 27 ACGTGAATTACGACGACCA 8

XX RESULT 3
XX ABK12019
XX ID ABK12019 standard; DNA; 32 BP.
XX AC ABK12019;
XX DT 05-JUN-2002 (first entry)
XX DE Human cyclin B2 related B1 anti-sense RT-PCR primer.
XX KW RT-PCR; primer; reverse transcriptase; ss; B1.
XX OS Homo sapiens.
XX PN KR99081550-A.
XX PD 15-NOV-1999.
XX PF 30-APR-1998; 98KR-00015566.
XX PR 30-APR-1998; 98KR-00015566.
XX PA (KIMD/) KIM D G.
XX PI Kim DG, Yoo GR, Shin HS;
XX WPI; 2000-617338/59.
XX DR

Best Local Similarity 84.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTGAATTATACCGCCA 20
| | | | | | | | | | | | | | | | | | | | | |
DB 35 CATGAATTATCCCGCCA 53

RESULT 6

ACD93498
ID ACD93498 standard; cDNA; 75 BP.

ACD93498;

23-SEP-2003 (first entry)

Human colon cancer cell expressed cDNA #1910.

Open reading frame detection; genome sequencing; colon cancer;
breast cancer; population genome analysis; genetic shift; cancer;
antibiotic resistance; antibiotic non-tolerance; congenital disease;
agriculture; food crop genome; resistance gene; retrovirus;
influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
gene; ss.

Homo sapiens.

US2002155438-A1.

24-OCT-2002.

27-SEP-1999; 99US-00406117.

20-NOV-1998; 98US-00196716.

(SIMP/) SIMPSON A J G.

(NETO/) NETO E D.

(BRENT/) BRENTANI R R.

Simpson AJG, Neto ED, Brentani RR;

WPI; 2003-182626/18.

Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.

Example 9; Page 297; 959pp; English.

The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a coding,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. Further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a fetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,

in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library

Sequence 75 BP; 14 A; 30 C; 9 G; 22 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 10; Length 75;
Best Local Similarity 84.2%; Pred. No. 2.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACGTGAATTATACCGCC 19
| | | | | | | | | | | | | | | | | | | | | |
DB 50 ACGTGAATTCTACCATCC 68

RESULT 7

ACIS8064/C
ID ACIS8064 standard; DNA; 25 BP.

ACIS8064;

13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 58055.

EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFRY-) AFRYMETRIX INC.

Miltmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58055; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-

blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 4 A; 4 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TGGAAATTATACCAAGCA 20
|||||
Db 25 TGGAAATTATACCAAGCA 9

RESULT 8

ACIS8692/c
ID ACIS8693 standard; DNA; 25 BP.

ACIS8693;

13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 58684.

EST; seq; probe; expressed sequence tag; microarray; gene expression;
genetic variation; biallelic marker; polymorphism; human;
cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFY-) AFFYMETRIX INC.

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58684; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by

primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 5 A; 4 C; 5 G; 11 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TGGAAATTATACCAAGCA 20
|||||
Db 24 TGGAAATTATACCAAGCA 8

RESULT 9

ACIS8692/c
ID ACIS8693 standard; DNA; 25 BP.

ACIS8692;

13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 58683.

EST; seq; probe; expressed sequence tag; microarray; gene expression;
genetic variation; biallelic marker; polymorphism; human;
cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFY-) AFFYMETRIX INC.

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58683; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been

CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 4 A; 4 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;
 Best Local Similarity 88.2%; Pred. No. 3.8e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TGGAAATTATACGAGCCA 20
 |||||
 DB 24 TCGAATTATACAGACA 8

RESULT 10

AA051108
 ID AA051108 standard; DNA; 29 BP.

XX AA051108;

DT 25-MAR-2003 (revised)
 DT 24-MAY-1994 (first entry)

XX Alpha subunit specific PCR primer for rat gustducin cDNA.

KM Taste modifying agent; ligand; antiligand; binding activity; taste;
 KM taste receptor cells; sweet; bitter; sweet; salty; sour; ss;
 amplification.

XX Synthetic.

XX WO9321337-A1.

XX 28-OCT-1993.

XX 08-APR-1993; 93WO-US003279.

XX 09-APR-1992; 92US-00868353.

XX (MARG/) MARGOLSKEE R F.

XX Margolskee RF;

XX WPI: 1993-351746/44.

XX P-PSDB; AAR42435.

XX New gustducin alpha subunit protein - used for identifying taste
 PT modifying agents which mimic or inhibit sweet, bitter, salty or sour
 PT tastes.

XX Disclosure; Page 12; 50pp; English.

XX Six degenerate oligonucleotide primer sets were made to correspond to
 CC regions of amino acids highly conserved among previously described G
 CC protein alpha subunits. The primers were used for PCR with DNA from a
 CC taste cell library as template. Partial clones and further PCR primers
 CC (shown) were used to isolate a composite gustatory alpha subunit clone or
 CC gustducin gene clone. See also AA051098-107. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 2; Length 29;
 Best Local Similarity 80.0%; Pred. No. 4.9e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ACGTGAATTATACGAGCCA 20
 |||||
 DB 9 ACGTTTAAATTATTCAGCCA 28

RESULT 11

AAV54426
 ID AAV54426 standard; cDNA; 29 BP.

XX AAV54426;

DT 21-DEC-1998 (first entry)

XX Nucleotide sequence of PCR primer 10.

KM PCR; primer; amplification; rat; gustducin alpha-subunit; taste;
 KM inhibition; ss.

XX Synthetic.

XX Rattus sp.

XX US5817759-A.

XX 06-OCT-1998.

XX 20-MAR-1995; 95US-00407804.

XX 09-APR-1992; 92US-00868353.

XX 08-APR-1993; 93US-00045801.

XX (LING-) LINGUAGEN CORP.

XX Margolskee RF;

XX WPI: 1998-556463/47.

XX New purified and isolated rat gustducin alpha-subunit polypeptide - can
 PT be delivered to taste receptor cells to modify taste, e.g. mimic or
 PT inhibit sweet and/or bitter tastes.

XX Example 1; Col 39-40; 25pp; English.

XX This is the nucleotide sequence of a PCR primer (derived from the
 CC conserved regions of rat gustducin) used for amplification in the method
 CC of the invention where the rat gustducin alpha-subunit protein used in
 CC the method of the invention to modify taste. The peptides or fragments
 CC can be delivered to taste receptor cells to modify taste, e.g. mimic or
 CC inhibit sweet and/or bitter tastes. The polypeptides can also be used in
 CC screening assays for taste-modifying agents

XX Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 2; Length 29;
 Best Local Similarity 80.0%; Pred. No. 4.9e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ACGTGAATTATACGAGCCA 20
 |||||
 DB 9 ACGTTTAAATTATTCAGCCA 28

RESULT 12
 AA249047
 ID AA249047 standard; DNA; 29 BP.

XX AA249047;

XX 31-MAR-2000 (first entry)

XX PCR primer for taste cell specific G protein.

KM PCR primer; taste cell specific G protein; taste modifying agent;
 KM gustducin; transducin; taste inhibitor; ss.

XX Rattus sp.

XX US6008000-A.

PD 28-DEC-1999.
XX
XX 28-JUL-1996; 98US-00124807.
XX
XX 09-APR-1992; 92US-00868353.
PR 20-MAR-1995; 95US-00407804.
XX
XX (LING-) LINGUAGEN CORP.
XX
XX Margolskee RF;
XX WPI; 2000-096373/08.
DR
PT Identifying taste modifying agents which can interact with taste
PT receptors to mimic or block natural taste stimulants.
XX
XX Example 1; Col 7; 25pp; English.
PS
XX This sequence represents a PCR primer used to isolate a rat taste cell
CC specific G protein. The invention relates to a method of identifying a
CC taste modifying agent, comprising: (a) incubating phospholipid vesicles
CC having gustducin alpha-subunit or transducin alpha-subunit and G protein
CC beta- and gamma-subunits associated in biologically active form with the
CC agent and GTPgammaS; and (b) determining the rate of GTPgammaS binding by
CC the alpha-subunit in comparison to a standard rate where an increase in
CC the rate of binding indicates that the agent is a taste stimulator and a
CC inhibitor. The method is useful for identifying taste modifying agents
CC which can interact with taste receptors to mimic, block or inhibit
CC particular tastes
CC
SQ Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 68.0%; Score 13.6; DB 3; Length 29;
XX Best Local Similarity 80.0%; Pred. No. 4.9e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 ACGTGAATTATACGACCA 20
DB 9 ACGTTAATTATTTCAGCCA 28
XX
XX RESULT 13
XX ABT15720
XX ID ABT15720 standard; DNA; 29 BP.
XX
XX ABT15720;
XX
XX 28-MAR-2003 (first entry)
XX
XX Human cancer/testis antigen PCR primer - SEQ ID No 11.
DE Human, PCR; primer; gene therapy; vaccine; cancer; cancer/testis antigen;
XX CT antigen; ss.
OS Homo sapiens.
XX
XX WO200278526-A2.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-US009808.
XX
XX 30-MAR-2001; 2001US-0280718P.
XX 20-APR-2001; 2001US-0285154P.
XX 05-OCT-2001; 2001US-0327432P.
XX 22-JAN-2002; 2002US-00054683.
XX
XX (LUDM-) LUDMIG INST CANCER RES.
XX (CORR) CORNELL RES FOUND INC.
XX Old LJ, Scanlan MJ, Chen Y;
XX

DR WPI; 2003-040608/03.
XX
XX Diagnosing cancer comprises contacting a biological sample isolated from
PT a subject with an agent that specifically binds to a nucleic acid
PT molecule, its expression product or fragment or an antibody that binds to
PT the product or fragment.
XX
XX Example 2; Page 68; 155pp; English.
PS
XX The invention comprises a method for diagnosing cancer, the method
CC involves detecting the DNA or protein sequences of human cancer/testis
CC (CT) antigens that are disclosed in the invention. The method of the
CC invention is useful for detecting/diagnosing, treating and monitoring a
CC cancer or condition characterized by the expression of a human CT
CC antigen. The present DNA sequence represents a PCR primer used in an
CC example of the invention
XX
SQ Sequence 29 BP; 7 A; 13 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 68.0%; Score 13.6; DB 8; Length 29;
XX Best Local Similarity 80.0%; Pred. No. 4.9e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 ACGTGAATTATACGACCA 20
DB 3 ACGTGAAGCTATACGACCA 22
XX
XX RESULT 14
XX ACA62089
XX ID ACA62089 standard; DNA; 29 BP.
XX
XX ACA62089;
XX
XX 19-AUG-2003 (first entry)
XX
XX G protein alpha subunit PCR primer #10.
DE
XX Taste; taste modification; gustducin alpha subunit;
XX ligand binding activity; antiligand binding activity;
XX G protein alpha subunit; conserved region; PCR; primer; ss.
XX
XX Synthetic.
XX
XX US2003013119-A1.
XX
XX 16-JAN-2003.
XX
XX 21-FEB-2001; 2001US-00789996.
XX
XX 09-APR-1992; 92US-00868353.
XX 08-APR-1993; 93US-00045801.
XX 20-MAR-1995; 95US-00407804.
XX 28-JUL-1998; 98US-00124807.
XX 20-OCT-1999; 99US-00421796.
XX
XX (LING-) LINGUAGEN CORP.
XX
XX Margolskee RF;
XX
XX WPI; 2003-466043/44.
XX
XX Novel gustducin alpha-subunit polypeptide possessing ligand/antiligand
PT binding activity or immunological property specific to gustducin, for
PT identifying peptide ligand/antiligand of gustducin and taste modifying
PT agent.
XX
XX Example 1; Page 4; 27pp; English.
PS
XX The invention describes a purified and isolated gustducin alpha subunit
CC polypeptide (1), fragment or variant possessing at least one
CC ligand/antiligand binding activity or immunological property specific to
CC gustducin. (1) is useful for identifying a peptide ligand/antiligand of

CC guestducin (1) with peptides and isolating peptides which
CC bind to (1), and for identifying taste modifying agent. An antibody is
CC useful for modifying taste which involves delivering Ab to taste receptor
CC cell. The antibody is useful for purifying (1) and for blocking or
CC inhibiting ligand/antiligand binding activities of guestducin. This
CC sequence represents a primer designed using a G protein conserved region
CC and used to create a primer for the construction of a G protein cDNA
CC library for isolation of guestducin
XX
SQ Sequence 29 BP; 8 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

Query Match	68.0%;	Score 13.6;	DB 9;	Length 29;
Best Local Similarity	80.0%;	Pred. No. 4.9e+03;		
Matches 16;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      1  ACGTGAATTATACCAGCCA  20
          ||||  |||||  |||||
Db      9  ACGTTTAATTATTTCAGCCA  28
```

RESULT 15

ID ADP09053 standard; DNA; 30 BP.

AC ADP09053;

DT 26-AUG-2004 (first entry)

DE PCR primer 54 used to genotype human chromogranin B polymorphism.

KW breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB;

KW single nucleotide polymorphism.

OS Homo sapiens.

PN WO2004047767-A2.

PD 10-JUN-2004

PF 25-NOV-2003; 2003WO-US037966.

PR 25-NOV-2002; 2002US-0429136P.

XX
XX
(STORY) STORYBOOK TWO

XX
XX

XX
XX
2004 441000 / 41

XX
XX

PT or absence of one or more nucleotide polymorphic variants
diagnosing preventing and/or treating breast cancer

XX
XX
XXXXX

CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a risk of breast cancer,
CC as well as therapeutic and prophylactic treatments that specifically
CC target breast cancer, such as gene therapy. The current sequence is that
CC of a PCR primer of the invention which was used to genotype single
CC nucleotide polymorphisms within human chromosome 8 (CH8B; secretogranin
CC 1; SG1) DNA which is located at chromosomal position 20pter-p12.

Sequence 30 BP; 8 A; 8 C; 7 G; 7 T; 0 U; 0 Other;

Query Match	Score	DB	Length
68.0%	13.6	12	30

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACCAGCCA 20
||| | | | | | | |
Db 1 ACGTTGATGAGACCAGCCA 20

Search completed: May 23, 2006, 11:01:29
Job time : 293 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:01:41 ; Search time 4305 Seconds
(without alignments)
259.788 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgfgaattacacagcca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 495048

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.8	84.0	69	14	BX230540 Danio rer
2	14.2	71.0	75	1	AI903657 OV-PR032-
3	13.8	69.0	69	4	CB552792 MMSPO038
4	13.6	68.0	70	14	AL771470 Arabidops
5	13.6	68.0	70	4	CD001979 C4B12 sub
6	13.2	66.0	63	13	CM131880 104_515_1
7	13.2	66.0	66	10	N71991 yz96D01.ai
8	13.2	66.0	69	13	DU440790 109842106
9	13.2	66.0	69	11	DU440790 109842106
10	13.2	66.0	75	12	AP149581 APL49581
11	12.8	64.0	63	1	AL732271 AL732271
12	12.8	64.0	71	8	CV303709 t963602.b
13	12.8	64.0	75	3	BU634669 016C12.in
14	12.6	63.0	45	11	AZ480835 1M0302109
15	12.6	63.0	56	6	AK219728 Mus muscu
16	12.6	63.0	60	13	CL308290 03F0096-0
17	12.6	63.0	65	10	DV237624 A2FLD67TO
18	12.6	63.0	67	11	AZ645226 1M0510403
19	12.6	63.0	69	10	DY249203 CSTFBLD07

20	12.6	63.0	72	12	CG466064 01S0542-0
21	12.6	63.0	72	14	AL757528 Arabidops
22	12.6	63.0	73	14	BX691027 Arabidops
23	12.4	62.0	54	5	CD530824 08C01 Ara
24	12.4	62.0	55	1	AJ235741 AJ235741
25	12.4	62.0	55	11	AZ658522 1M0535A18
26	12.4	62.0	59	13	CM391650 f8db001f0
27	12.4	62.0	60	8	CN931823 000428AF8
28	12.4	62.0	72	14	BX290465 Arabidops
29	12.2	61.0	49	1	AI424311 t690D05.X
30	12.2	61.0	55	1	AM085274 AM085274
31	12.2	61.0	57	11	BH847350 SALK_0528
32	12.2	61.0	56	14	CR360294 Arabidops
33	12.2	61.0	62	14	AJ595367 Arabidops
34	12.2	61.0	62	14	CR009942 Reverse s
35	12.2	61.0	63	5	CD948686 SAG_22 Ge
36	12.2	61.0	63	11	BH790863 SALK_0580
37	12.2	61.0	64	13	CL210752 F023F03 G
38	12.2	61.0	67	14	AJ622651 Drosophi1
39	12.2	61.0	67	14	CR397249 Arabidops
40	12.2	61.0	69	1	AA449410 zxc04f12.x
41	12.2	61.0	69	3	BP075817 BP075817
42	12.2	61.0	69	11	AZ826432 2M0102112
43	12.2	61.0	70	2	BF779346 3179-63 h
44	12.2	61.0	71	8	C0745478 TGESTZPD0
45	12.2	61.0	72	11	BZ354686 SALK_1256

ALIGNMENTS

RESULT 1
LOCUS BX230540 69 bp DNA linear GSS 29-JAN-2003
DEFINITION Danio rerio genomic clone DKEX-253D18, genomic survey sequence.
ACCESSION BX230540
VERSION BX230540.1 GI:28064690
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 69)
Humphray, S.J., Huckle, E. and Durham, J.L.
AUTHORS Direct Submission
TITLE Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
JOURNAL Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humphrey@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 253D18, 253D18
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
source location/Qualifiers
1..69
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-253D18"
/tissue_type="Testis"
/note="Vector pIndigoBAC-536"
ORIGIN
Query Match 84.0%; Score 16.8; DB 14; Length 69;
Best Local Similarity 90.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 ACGTGAATTATACAGCCA 20
DB 50 ACATGCAATTATACAGCCA 69
RESULT 2

AI903657 75 bp mRNA linear EST 30-MAR-2000
 LOCUS AI903657
 DEFINITION QV-BT032-190299-122 BT032 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AI903657
 VERSION AI903657.1 GI:6494044
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 75)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zagro, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 JOURNAL
 PUBMED
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/seq/gethtml.pl?ti=QVet2-QV-BT032-122.html
 kt3=190299&ct=1)
 Seq primer: puc 18 forward.
 Location/Qualifiers
 1..75
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="Adult"
 /clone_lib="BT032"
 /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
 SmaI. A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN
 Query Match 71.0%; Score 14.2; DB 1; Length 75;
 Best Local Similarity 84.2%; Pred. No. 1.7e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ACGTGAATTATACGACC 19
 Db 50 ACCTGGAATTCACCATCC 68

RESULT 3
 CB552792 69 bp mRNA linear EST 01-JUN-2003
 LOCUS CB552792
 DEFINITION MMSF0038_E07 MMSF Macaca mulatta cDNA, mRNA sequence.
 ACCESSION CB552792
 VERSION CB552792.1 GI:31301987
 KEYWORDS EST.
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecidae; Macaca.

REFERENCE 1 (bases 1 to 69)
 AUTHORS Katze, M.G., Bumgarner, R., Korch, M., Feldman, R., Amjadi, M. and
 Holzman, T.
 TITLE Expressed sequence tags from Rhesus macaque spleen
 JOURNAL Unpublished (2002)
 COMMENT Contact: Holzman T
 Katze Lab
 University of Washington
 Box 358070, Seattle, WA 98195-8070, USA
 Tel: 206 732 6156
 Fax: 206 732 6035
 Email: ted@locke.hs.washington.edu
 Similar to GenBank entry HSM804066 AL832755 Homo sapiens mRNA; cDNA
 DKFZp686A0927 (from clone DKFZp686A0927). 7/2002
 Plate: MMSF0038 row: E column: 07.
 FEATURES
 source
 1..69
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /db_xref="taxon:9544"
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 /cell_type="monocytes"
 /dev_stage="adult"
 /clone_lib="MMSF"
 /note="Organ: spleen"

ORIGIN
 Query Match 69.0%; Score 13.8; DB 4; Length 69;
 Best Local Similarity 88.2%; Pred. No. 2.7e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 TGAATTATACGACCA 20
 Db 40 TGAAGTACTACGCA 24

RESULT 4
 AL771470 69 bp DNA linear GSS 01-APR-2004
 LOCUS AL771470
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-180E10-013611,
 genomic survey sequence.
 ACCESSION AL771470
 VERSION AL771470.1 GI:21533672
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
 GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)
 12874060
 2
 Rosso, M.G., Li, Y., Strizhov, N., Reise, B., Dekker, K. and
 Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 14756321
 3
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
 Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 14682050
 4 (bases 1 to 69)
 Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
 Direct Submission

JOURNAL
COMMENT

Submitted (31-MAR-2004) Welschaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany. This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F1B16. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source

Location/Qualifiers

1..69

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

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/clone="CGK-180B10-013611"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (71) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The

lines contain one or more T-DNA insertions. The DNA

fragment(s) resulting from the PCR were directly sequenced

to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed."

ORIGIN

Query Match 68.0%; Score 13.6; DB 14; Length 69;

Best Local Similarity 80.0%; Pred. No. 3.4e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATTCAGCCA 20
17 ACGAGAAATTGACCGCTA 36

LOCUS CD001979 70 bp mRNA linear EST 01-MAY-2003
DEFINITION C4B12 subtracted cochlea cDNA library Homo sapiens cDNA, mRNA
sequence.
ACCESSION CD001979
VERSION CD001979.1 GI:30307306
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 70)
Luijendijk,M.W.J., van de Pol,T.J.R., van Duinhoven,G., den
Hollander,A.I., ten Caat,J., van Limpe,V., Brunner,H.G., Kremer,H.
and Cremers,F.P.M.
Cloning, characterization and mRNA expression of novel human fetal
cochlea cDNAs
Unpublished (2003)
Contact: Kremer H
Department of Human Genetics
University Medical Center Nijmegen
P.O. Box 9101, 6500 HB Nijmegen, The Netherlands
Tel: +31 24 3614017
Fax: +31 24 3540488
Email: h.kremer@umcn.nl
The insert was not completely sequenced
Insert Length: 70 Std Error: 0.00
Seq primer: 17 GTAAATGAGACTCATTATAGCGGG
POLYA=No.

FEATURES

source

Location/Qualifiers

1..70

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="Cochlea"

ORIGIN

Query Match 68.0%; Score 13.6; DB 4; Length 70;

Best Local Similarity 80.0%; Pred. No. 3.5e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATTCAGCCA 20
3 ACTTGAAATATTCAGCCA 22

RESULT 6
LOCUS CW131880/c 63 bp DNA linear GSS 29-OCT-2004
DEFINITION 104_515_11115912_116_34797_096 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 1115912, genomic survey
sequence.
ACCESSION CW131880
VERSION CW131880.1 GI:54824427
KEYWORDS GSS.
SOURCE
ORGANISM Sorghum bicolor (sorghum)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Sorghum.
1 (bases 1 to 63)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McWenamy,D., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korff,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
Plos Biol. 3 (1), e13 (2005)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 515 row: a column: 24
Seq primer: T3 Reverse
Class: methylation filtered
High quality sequence stop: 63.

FEATURES

source

1..63

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="RTx623"

/db_xref="taxon:4558"

/clone="11115912"

/clone_lib="Sorghum methylation filtered library (LibID:
104)"

/note="Organ: leaf; Vector: pGSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pGSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN

	Query Match	66.0%;	Score 13.2;	DB 13;	Length 63;
	Best Local Similarity	83.3%;	Fred. NO. 5.6e+04;		
	Matches 15,	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Oy	3 GTGGATATTATACCGCCA 20				
Db	23 GTCRAATTATACAGCCA 6				
RESULT 7	N71991	66 bp	mRNA	linear	EST 15-MAR-1996
LOCUS	N71991				
DEFINITION	y296b01.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290857 3'				
	INHIBITORY FACTOR (HUMAN); mRNA sequence.				
ACCESSION	N71991				
VERSION	N71991.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 66)				
AUTHORS	Hillier,M., Clark,N., Dubnue,T., Elliston,K., Hawkins,M., Holman,M., Hulman,M., Kueba,T., Le,M., Lennon,G., Marra,M., Paterson,J., Rifkin,J., Rohlfing,T., Soares,M., Tan,F., Tivvaskis,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.				
TITLE	The WashU-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: m13 -40 forward High quality sequence stop: 1. Location/Qualifiers 1. 66 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:3883987" /db_xref="taxon:9606" /clone="IMAGE:290857" /sex="Male" /tissue_type="melanocyte" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares melanocyte 2NbHM" /note="Vector: pRTT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCACTGTGAAGTGAGCGGCCGCAGATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRTT3 vector (Pharmacia). Library constructed by Bento Soares and M.Patim Bonaalido. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."				
FEATURES	source				
ORIGIN	Query Match	66.0%;	Score 13.2;	DB 10;	Length 66;
	Best Local Similarity	78.9%;	Pred. NO. 5.6e+04;		
	Matches 15;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
OY	1 ACGTGGATTATACAGCC 19				
DB	42 AGGTGAGTGTTCACGCC 60				

RESULT 8	DU440790	66 bp	DNA	linear	GSS 06-OCT-2005
LOCUS	DU440790				
DEFINITION	1098421061035 CHORI-243 Ovis aries genomic clone CH243-244P19,				
ACCESSION	DU440790				
VERSION	DU440790.1	GI:77194680			
KEYWORDS					
ORGANISM	Ovis aries (sheep)				
SOURCE	Ovis aries				
REFERENCE	1 (bases 1 to 66)				
AUTHORS	Kirkness, E., Shetty, J., de Jong, P., McEwan, J. C., Odely, H. and Cockett, N.				
TITLE	Ovine BAC End Sequences from Library CHORI-243				
JOURNAL	Unpublished (2004)				
COMMENT	Other GSSs: 1098415783056 Contact: Ewen Kirkness The Institute for Genomic Research (TIGR; www.tigr.org) 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-795-7536 Email: ekirknes@tigr.org Sequences generated at the J. Craig Venter Institute Joint Technology Center (JCVJTC; http://www.venterlinstitute.org/). Original Trace: 1098421061035 Trace Tr: gnl ci 918984658 Insert Length: 184000 Std Error: 0.00 row: P column: 19 Seq primer: T7 Class: BAC ends. Location/Qualifiers 1. .66 /organism="Ovis aries" /mol_type="genomic DNA" /strain="rexel breed" /db_xref="taxon:9940" /clone="CH243-244P19" /sex="Male" /cell_type="Blood" /clone_lib="CHORI-243" /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; The CHORI-243 sheep (M) (Ovis aries) BAC library produced by Pieter de Jong's lab at CHORI http://bacpac.chori.org/library.php?id=162"				
ORIGIN					
Query Match	66.0%;	Score 13.2;	DB 13;	Length 66;	
Best Local Similarity	83.3%;	Pred. No. 5.6e+04;			
Matches	15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	3 GTGGAATTATACCGACA 20				
DB	29 GTGACCTTTTACGACGA 46				
RESULT 9	AF149581/c	69 bp	DNA	linear	GSS 12-JUN-2000
LOCUS	AF149581				
DEFINITION	AF149581 Human chromosome 18q21 from exon-trapping Homo sapiens				
ACCESSION	AF149581				
VERSION	AF149581.1	GI:8485912			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 69)				
AUTHORS	Chen, H., Huo, Y., Patel, S., Zhu, X., Swift-Scanlan, T., Reeves, R. H., DePaeto, R. Jr., Ross, C. A. and McIntosh, M. G.				

TITLE Gene identification using exon amplification on human chromosome 18q21: implications for bipolar disorder
JOURNAL Mol. Psychiatry 5 (5), 502-509 (2000)
PUBMED 11032383
COMMENT Contact: Chen H
Psychiatry and Behavioral Sciences
Johns Hopkins University School of Medicine
600 N. Wolfe Street, Baltimore, MD 21287, USA
Email: hchow@chlink.welch.jhu.edu
Class: exon-trapped.

FEATURES
source
1..69
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="18q21"
/clone="3a19"
/clone_11b="Human chromosome 18q21 from exon-trapping"

ORIGIN
Query Match 66.0%; Score 13.2; DB 11; Length 69;
Best Local Similarity 83.3%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACGAC 18
|||||
45 ACGTGAATTATTCATC 28
|||||

RESULT 10
CC155989
LOCUS XST053 BayGenomics Gene Trap Library pGT2TmPfs Mus musculus cDNA,
mRNA sequence.
DEFINITION CC155989.1 GI:30109345
GSS.
ACCESSION CC155989.1 GI:30109345
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 75)
BayGenomics.
AUTHORS
TITLE http://baygenomics.ucsf.edu/cgi-bin/baysearch.py?OPTION=EXACT&TYPE=Unpublished (2001)
JOURNAL Contact: BayGenomics
COMMENT Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from
http://baygenomics.ucsf.edu/cgi-bin/baysearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=XST053
Class: Gene Trap

FEATURES
source
1..75
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_11b="BayGenomics Gene Trap Library pGT2TmPfs"
/note="Vector: pGT2TmPfs"

ORIGIN
Query Match 66.0%; Score 13.2; DB 12; Length 75;
Best Local Similarity 83.3%; Pred. No. 5.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTGAATTATACGACC 19

Db 46 CGTGAATTATACGACC 63
|||||

RESULT 11
AL732271 63 bp mRNA linear EST 07-MAY-2002
LOCUS AL732271 pool_AK_11b_v_SPE Homo sapiens cDNA, mRNA sequence.
DEFINITION AL732271
ACCESSION AL732271
VERSION AL732271.1 GI:20501682
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 63)
Ashcroft,K., Bethel,G., Bye,J.M., Howell,G.R., Huckle,E.J. and Sheridan,E.
AUTHORS
TITLE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name: sc0d10643.158623Sa
Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute's program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from a pool_AK_11b_v_SPE cDNA library. Further information can be found at
http://www.sanger.ac.uk/Teams/Team69/
Location/Qualifiers

FEATURES
source
1..63
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="20"
/clone_11b="pool_AK_11b_v_SPE"

ORIGIN
Query Match 64.0%; Score 12.8; DB 1; Length 63;
Best Local Similarity 87.5%; Pred. No. 9.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACCA 16
|||||
34 ACGTGAATTTCACCA 49
|||||

RESULT 12
CV303709 71 bp mRNA linear EST 23-SEP-2004
LOCUS tg63e02.b7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA
DEFINITION CV303709
ACCESSION CV303709.1 GI:52621042
VERSION
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 71)
Dike,S., Balija,V.S., Nascimeto,L.U., Xuan,Z., Ou,J., Zulaevn,T., Palmer,L.E., Hannon,G., Zhang,M.O. and McCombe,W.R.
AUTHORS
TITLE The mouse genome: Experimental examination of gene predictions and
JOURNAL transcripitional start sites
PUBMED Genome Res. 14 (12), 2424-2429 (2004)
COMMENT 15574821
Contact: Balija VS

McCombie Laboratory
Cold Spring Harbor Laboratory
500 Sunnyside Blvd, Woodbury, NY 11797, USA
Fax: 516 422 4109
Email: balija@csnl.org.
Location/Qualifiers

FEATURES
source

1..75
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_1lb="Mouse 5' RACE clones"
/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments amplified from 5' RACE cDNA generated from 15 pooled mouse tissues and stages: 7, 11, 15, & 17-day total embryo, whole brain, eye, kidney, liver, lung, prostate, and submaxillary gland, smooth muscle, spleen, testes and uterus."

ORIGIN

Query Match 64.0%; Score 12.8; DB 8; Length 71;
Best Local Similarity 87.5%; Pred. No. 9.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 TGAATTATACCAGCC 19
13 TGGCATGTGACCAGCC 28

RESULT 13
B0634669 75 bp mRNA linear EST 23-SEP-2002
DEFINITION 016C12 Infected Arabidopsis leaf Arabidopsis thaliana cDNA, mRNA
sequence.

ACCESSION B0634669
VERSION B0634669.1 GI:23301924
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 75)
Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S. and Wellinder K.G.

REFERENCE
EST sequencing of Erysiphe cichoracearum infected Arabidopsis plants

TITLE
Unpublished (2002)

JOURNAL
COMMENT
Contact: Karen G. Wellinder
Institute for Biotechnology
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk.

FEATURES
source

1..75
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/dev_stage="Plant 3 weeks old, three days post infection"
/clone_1lb="Infected Arabidopsis leaf"
/note="Organ: leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."

ORIGIN

Query Match 64.0%; Score 12.8; DB 3; Length 75;
Best Local Similarity 87.5%; Pred. No. 9.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 TGAATTATACCAGCC 19
6 TGAAGTATACCAGCC 21

RESULT 14
A2480835 45 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0302109R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0302109 R, genomic survey sequence.

ACCESSION A2480835
VERSION A2480835.1 GI:10641900
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedernhausen,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: 1 column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers

FEATURES
source

1..45
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0302109"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (91[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.0%; Score 12.6; DB 11; Length 45;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 CGTGAATTATACCAAGCA 20
 |||||
 21 CGGGAGATCTTACCAAGCA 39

RESULT 15

AK219728 56 bp mRNA linear HTC 23-NOV-2004
 LOCUS AK219728/c

DEFINITION Mus musculus cDNA, clone:Y2G0149G13, strand:minus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000069765, based on BLAT search.

ACCESSION

AK219728

VERSION AK219728.1 GI:56043905

KEYWORDS HTC; ASSETS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1

Marahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayashizaki, Y. and Carninci, P.

Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas

Nat. Methods 1, 233-239 (2004)

2 (bases 1 to 56)

Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N., Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M., Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watanahiki, A. and Hayashizaki, Y.

Direct Submission

Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT

Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pFLCI vector. (Reference).

FEATURES

source

1.56
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="Y2G0149G13"
 /cell_line="mixture of B16-F10Y and melan-c"
 /cell_type="mixture of melanoma cell and melanocyte cell"
 /clone_lib="Alternative Splicing Library L3"
 /note="strand:minus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000069765, based on BLAT search"

ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 56;
 Best Local Similarity 78.9%; Pred. No. 1.1e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 1 ACGTGAATTATACCAAGCC 19
 |||||
 29 AAGTGAAGTATACCAAGCC 11

Search completed: May 23, 2006, 12:54:23
 Job time : 4309 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:29:33 ; Search time 68 Seconds
(without alignments)
550.326 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtgacttatacagcaca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 1518026

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCtUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	50	US-10-131-827-1716	Sequence 1716, Ap
2	14.2	71.0	50	US-10-131-831-1716	Sequence 1716, Ap
3	14.2	71.0	68	US-08-956-171E-2684	Sequence 2684, Ap
4	14.2	71.0	68	US-08-781-968A-2684	Sequence 2684, Ap
5	13.8	69.0	25	US-09-396-196G-39721	Sequence 39721, A
6	13.6	68.0	29	US-07-868-353A-34	Sequence 34, Appl
7	13.6	68.0	29	US-08-407-804-43	Sequence 43, Appl
8	13.6	68.0	29	US-09-124-807-43	Sequence 43, Appl
9	13.6	68.0	45	US-08-233-009-43	Sequence 43, Appl
10	13.4	67.0	25	US-09-396-196G-80092	Sequence 80092, A
11	13.4	67.0	25	US-09-396-196G-80093	Sequence 80093, A
12	13.4	67.0	25	US-09-396-196G-116886	Sequence 116886, A
13	12.8	64.0	20	US-09-844-552A-85	Sequence 85, Appl
14	12.8	64.0	21	US-08-410-784A-7	Sequence 7, Appl
15	12.8	64.0	21	US-10-179-562-41	Sequence 41, Appl
16	12.8	64.0	24	US-09-564-357-13	Sequence 41, Appl
17	12.8	64.0	29	US-09-304-232-817	Sequence 817, App
18	12.6	63.0	27	US-07-945-156A-4	Sequence 4, Appl
19	12.6	63.0	42	US-08-610-728B-8	Sequence 8, Appl
20	12.4	62.0	25	US-09-396-196G-123214	Sequence 123214, Appl
21	12.2	61.0	22	US-08-253-030-26	Sequence 26, Appl
22	12.2	61.0	24	US-09-947-770-32	Sequence 32, Appl
23	12.2	61.0	25	US-09-217-101-5	Sequence 5, Appl

24	12.2	61.0	25	3	US-09-577-005-62	Sequence 62, Appl
25	12.2	61.0	30	3	US-08-513-968-69	Sequence 69, Appl
26	12.2	61.0	30	3	US-09-576-160B-20	Sequence 20, Appl
27	12.2	61.0	30	3	US-09-576-160B-24	Sequence 24, Appl
28	12.2	61.0	40	2	US-08-399-696-31	Sequence 31, Appl
29	12.2	61.0	73	2	US-08-282-030-18	Sequence 18, Appl
30	12.2	61.0	73	7	PCT-US95-10219-18	Sequence 18, Appl
31	12	60.0	30	2	US-09-038-227-45	Sequence 45, Appl
32	12	60.0	50	2	US-08-171-388-478	Sequence 478, App
33	12	60.0	50	2	US-08-123-936-478	Sequence 478, App
34	12	60.0	50	2	US-08-475-228A-478	Sequence 478, App
35	12	60.0	50	3	US-08-482-080A-478	Sequence 478, App
36	12	60.0	50	3	US-09-354-947-478	Sequence 478, App
37	12	60.0	50	3	US-09-993-346-478	Sequence 478, App
38	12	60.0	50	3	US-10-131-827-982	Sequence 982, App
39	12	60.0	50	5	US-10-131-831-982	Sequence 982, App
40	12	60.0	50	7	PCT-US93-12388-478	Sequence 478, App
41	12	60.0	71	3	US-08-255-236-18	Sequence 18, App
42	12	60.0	71	3	US-09-123-728-34	Sequence 34, Appl
43	11.8	59.0	20	3	US-09-198-452A-6355	Sequence 6355, Ap
44	11.8	59.0	25	3	US-09-396-196G-113221	Sequence 113221, Appl
45	11.8	59.0	26	7	PCT-US92-06821A-25	Sequence 25, Appl

ALIGNMENTS

```
RESULT 1
US-10-131-827-1716
; Sequence 1716, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131, 827
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1716
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1716
Query Match          71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy      1 ACGTGAAATTATACAGCC 19
      |||||
Db      19 ACGTGAATTATACAGAC 37
      |||||
RESULT 2
US-10-131-831-1716
; Sequence 1716, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
```

```
FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1716
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-831-1716

Query Match      71.0%; Score 14.2; DB 5; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ACGTGGAATTATACGACC 19
Db      19 ACGTGGAATTATATCGAC 37

RESULT 3
US-08-956-171E-2684
Sequence 2684, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gill H. Choi
Patrick S. Dillon
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2684:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TITLE OF INVENTION: Methods of Genetic Analysis
CURRENT APPLICATION NUMBER: US/08-956-171E-2684

US-08-956-171E-2684

Query Match      71.0%; Score 14.2; DB 3; Length 68;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CGTGGAATTATACGACCA 20
Db      35 CATGGAATTATCCGCGCA 53

RESULT 4
US-08-781-986A-2684
Sequence 2684, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunach
Gill H. Choi
Patrick S. Dillon
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2684:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-2684

Query Match      71.0%; Score 14.2; DB 3; Length 68;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CGTGGAATTATACGACCA 20
Db      35 CATGGAATTATCCGCGCA 53

RESULT 5
US-09-396-196G-39721
Sequence 39721, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
David Mack
APPLICANT: David Lockhart
APPLICANT: Affimetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
CURRENT APPLICATION NUMBER: US/09/396,196G
```

;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FASTSeq for Windows Version 4.0
;; SEQ ID NO 39721
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-396-196G-39721

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGAATTATTCAGCCA 20
DB 1 TGAATTATTCAGCCA 17

RESULT 6
US-07-868-353A-34
; Sequence 34, Application US/07868353A
; Patent No. 5688662
; GENERAL INFORMATION:
; APPLICANT: Margolskee, Robert F.
; TITLE OF INVENTION: Guaducuin Materials and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; TELEFAX: (312) 474-0448
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/868,353A
; FILING DATE: 19920409
; CLASSIFICATION: 350
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5688662and, Greta E.
; REGISTRATION NUMBER: P-35,302
; REFERENCE/DOCKET NUMBER: 28038/30793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-868-353A-34

Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAAATTATTCAGCCA 20
DB 9 ACGTTTAATTATTCAGCCA 28

RESULT 7

US-08-407-804-43
; Sequence 43, Application US/08407804
; Patent No. 5817759
; GENERAL INFORMATION:
; APPLICANT: Margolskee, Robert F.
; TITLE OF INVENTION: Guaducuin Materials and Methods
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,804
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,801
; FILING DATE:
; APPLICATION NUMBER: US 07/868/353

ATTORNEY/AGENT INFORMATION:
; NAME: No. 5817759and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-407-804-43

Query Match 68.0%; Score 13.6; DB 2; Length 29;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAAATTATTCAGCCA 20
DB 9 ACGTTTAATTATTCAGCCA 28

RESULT 8
US-09-124-807-43
; Sequence 43, Application US/09124807
; Patent No. 6008000
; GENERAL INFORMATION:
; APPLICANT: Margolskee, Robert F.
; TITLE OF INVENTION: Guaducuin Materials and Methods
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/407,804
FILING DATE:
APPLICATION NUMBER: US 07/868/353
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6008000and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-124-807-43

Query Match 68.0%; Score 13.6; DB 3; Length 29;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGATTTATACGACCA 20
DB 9 ACGTTTATTTATTTACGCA 28

RESULT 9
US-08-233-009-43/c
Sequence 43, Application US/08233009
Patent No. 5646156
GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Johnson, Robert G
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INHIBITION OF EOSINOPHIL
TITLE OF INVENTION: ACTIVATION THROUGH A3 ADENOSINE RECEPTOR ANTAGONISM
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O.Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 25-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19219
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-233-009-43

Query Match 68.0%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGATTTATACGACCA 20
DB 32 ACCGAGATGACACCGACCA 13

RESULT 10
US-09-396-196G-80092/c
Sequence 80092, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80092
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-80092

Query Match 67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTGGATTTATACG 17
DB 18 GTGGAGATTTATACG 4

RESULT 11
US-09-396-196G-80093/c
Sequence 80093, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80093
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-80093

Query Match 67.0%; Score 13.4; DB 3; Length 25;
-Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTGGAATTATACCAG 17
|||
Db 15 GTGGAAGTATACCAG 1

RESULT 12
US-09-396-196G-116886/C
; Sequence 116886, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116886
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-116886

Query Match 67.0%; Score 13.4; DB 3; Length 25;
-Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGGAAATTATACCAG 18
|||
Db 25 TGGAAITTCACAGC 11

RESULT 13
US-09-844-525A-85
; Sequence 85, Application US/09844525A
; Patent No. 6468796
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BIFUNCTIONAL APOPTOSIS REGULATOR EXPRESSION
; FILE REFERENCE: RTS-0230
; CURRENT APPLICATION NUMBER: US/09/844,525A
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-844-525A-85

Query Match 64.0%; Score 12.8; DB 3; Length 20;
-Best Local Similarity 87.5%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTGGAATTATACCAG 18
|||
Db 1 GTGTAATTATACCTGC 16

RESULT 14
US-08-410-784A-7

; Sequence 7, Application US/08410784A

; Patent No. 5912413

; GENERAL INFORMATION:

; APPLICANT: MYERS, ALAN M.

; APPLICANT: JAMES, MARTHA G.

; TITLE OF INVENTION: ISOLATION OF SU1, A STARCH DEBRANCHING

; TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE

; TITLE OF INVENTION: SUGARY 1

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Weingarten, Schurgin, Gagnebin and Hayes LLP

; STREET: Ten Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/410,784A

; FILING DATE: 24-MAR-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Heine, Ph.D., Holliday C

; REGISTRATION NUMBER: 34,346

; REFERENCE/DOCKET NUMBER: ISU-002XX

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-2290

; TELEFAX: 617-451-0313

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

US-08-410-784A-7

Query Match 64.0%; Score 12.8; DB 2; Length 21;
-Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAATTATACCAGCA 20
|||
Db 1 GGGATCATACAGCCA 16

RESULT 15
US-10-179-562-41
; Sequence 41, Application US/10179562
; Patent No. 6995300
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; APPLICANT: James, Martha G.
; TITLE OF INVENTION: ISOLATION OF SU1, A STARCH DEBRANCHING
; TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE SUGARY 1
; FILE REFERENCE: ISU-002BX
; CURRENT APPLICATION NUMBER: US/10/179,562
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/256,741
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 43

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Zea mays
us-10-179-562-41
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Query Match          64.0%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      5 GGAATTATACCGCCA 20
          |||||
Db      1 GGGATCATACCGCCA 16
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Search completed: May 23, 2006, 11:37:08
Job time : 69 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:36:27 ; Search time 978 Seconds
(without alignments)
251.281 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtggaattaccagcca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24330200

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	Published Applications NA Main:
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3: /EMC Celerra SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*	
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16: /EMC Celerra SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-10-714-796-122
2	15.2	76.0	40	9	US-10-476-597-63
3	14.8	74.0	25	8	US-10-719-956-197295
4	14.8	74.0	25	9	US-10-719-900-135431
5	14.8	74.0	25	9	US-10-719-900-265411
6	14.8	74.0	50	16	US-11-175-859-7489
7	14.8	74.0	50	16	US-11-175-859-91821
8	14.4	72.0	25	9	US-10-719-900-962131
9	14.2	71.0	25	8	US-10-719-956-169821
10	14.2	71.0	25	8	US-10-719-956-169822
11	14.2	71.0	25	9	US-10-719-900-467341
12	14.2	71.0	25	10	US-10-956-157-15043
13	14.2	71.0	25	10	US-10-956-157-15044
14	14.2	71.0	25	10	US-10-956-157-190558
15	14.2	71.0	25	11	US-10-932-162A-135456
16	14.2	71.0	25	11	US-10-934-048A-39340
17	14.2	71.0	25	11	US-10-934-048A-78871

18	14.2	71.0	25	13	US-11-036-317-429637	Sequence 429637, Ap
19	14.2	71.0	50	7	US-10-131-827-1716	Sequence 1716, Ap
20	14.2	71.0	68	2	US-08-781-986A-2684	Sequence 2684, Ap
21	14.2	71.0	68	8	US-10-329-624-2684	Sequence 2684, Ap
22	14.2	71.0	19	14	US-11-083-784-274670	Sequence 274670, Ap
23	14.2	71.0	19	14	US-11-083-784-401583	Sequence 401583, Ap
24	14.2	71.0	19	14	US-11-083-784-401591	Sequence 401591, Ap
25	14.2	71.0	19	15	US-11-101-244-274670	Sequence 274670, Ap
26	14.2	71.0	19	15	US-11-101-244-401583	Sequence 401583, Ap
27	14.2	71.0	19	15	US-11-101-244-401591	Sequence 401591, Ap
28	14.2	71.0	19	15	US-10-843-527-45153	Sequence 45153, Ap
29	14.2	71.0	25	10	US-10-843-527-193024	Sequence 193024, Ap
30	13.8	69.0	18	11	US-10-310-914A-745552	Sequence 745552, Ap
31	13.8	69.0	19	11	US-10-310-914A-137469	Sequence 137469, Ap
32	13.8	69.0	19	14	US-11-083-784-274031	Sequence 274031, Ap
33	13.8	69.0	19	14	US-11-083-784-274065	Sequence 274065, Ap
34	13.8	69.0	19	14	US-11-083-784-274126	Sequence 274126, Ap
35	13.8	69.0	19	14	US-11-083-784-274153	Sequence 274153, Ap
36	13.8	69.0	19	15	US-11-101-244-274031	Sequence 274031, Ap
37	13.8	69.0	19	15	US-11-101-244-274065	Sequence 274065, Ap
38	13.8	69.0	19	15	US-11-101-244-274126	Sequence 274126, Ap
39	13.8	69.0	19	15	US-11-101-244-274153	Sequence 274153, Ap
40	13.8	69.0	25	6	US-10-098-263B-58055	Sequence 58055, Ap
41	13.8	69.0	25	6	US-10-098-263B-58683	Sequence 58683, Ap
42	13.8	69.0	25	6	US-10-098-263B-58684	Sequence 58684, Ap
43	13.8	69.0	25	8	US-10-681-773-29903	Sequence 29903, Ap
44	13.8	69.0	25	8	US-10-681-773-40933	Sequence 40933, Ap
45	13.8	69.0	25	8	US-10-681-773-58064	Sequence 58064, Ap

ALIGNMENTS

RESULT 1	US-10-714-796-122	Sequence 122, Application US/10714796
Publication No.	US20040180847A1	
GENERAL INFORMATION:		
APPLICANT:	Dobie, Kenneth W.	
APPLICANT:	Koller, Erich	
TITLE OF INVENTION:	ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION	
FILE REFERENCE:	ISHT-1004	
CURRENT APPLICATION NUMBER:	US/10/714,796	
CURRENT FILING DATE:	2003-11-17	
PRIOR APPLICATION NUMBER:	US 10/156,603	
PRIOR FILING DATE:	2002-05-23	
NUMBER OF SEQ ID NOS:	237	
SOFTWARE:	PatentIn version 3.2	
SEQ ID NO 122		
LENGTH:	20	
TYPE:	DNA	
ORGANISM:	Homo sapiens	
US-10-714-796-122		
Query Match	100.0%; Score 20; DB 9; Length 20;	
Best Local Similarity	100.0%; Pred. No. 3.5;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ACGTGAATTATACAGCCA 20	
DB	1 ACGTGAATTATACAGCCA 20	
RESULT 2	US-10-476-597-63/c	Sequence 63, Appl
Publication No.	US2004023576A1	
GENERAL INFORMATION:		
APPLICANT:	Bullard, James	
APPLICANT:	Danjic, Nebojsa	
APPLICANT:	McHenry, Charles S.	
TITLE OF INVENTION:	System for Discovery of Agents that Block Yersinia Pestis and	
TITLE OF INVENTION:	Pseudomonas Aeruginosa DNA Replication	

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FILE REFERENCE: RDYN.02/PCT-US
; CURRENT APPLICATION NUMBER: US/10/476,597
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/290,725
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: PCT/US02/15111
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/332,644
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 63
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-476-597-63
```

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Query Match          76.0%; Score 15.2; DB 9; Length 40;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 ACGTGAATTATACGACCA 20
        |||||
Db      27 ACGTGAATTACGACCA 8
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```
RESULT 3
US-10-719-956-197295/C
; Sequence 197295, Application US/10719956
; Publication No. US20040146910A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
```

```
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
```

```
; FILE REFERENCE: 3527.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,956
```

```
; CURRENT FILING DATE: 2003-11-20
```

```
; PRIOR APPLICATION NUMBER: 60/427,836
```

```
; PRIOR FILING DATE: 2002-11-20
```

```
; NUMBER OF SEQ ID NOS: 699466
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 197295
```

```
; LENGTH: 25
```

```
; TYPE: DNA
```

```
; ORGANISM: Rattus norvegicus
```

```
US-10-719-956-197295
```

```
Query Match          74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GTGGAATTATACGACCA 20
        |||||
Db      19 GTGGAATATACGACCA 2
```

```
RESULT 4
US-10-719-900-135431
```

```
; Sequence 135431, Application US/10719900
```

```
; Publication No. US20050026164A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
```

```
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
```

```
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
```

```
; CURRENT FILING DATE: 2003-11-20
```

```
; PRIOR APPLICATION NUMBER: 60/427,808
```

```
; PRIOR FILING DATE: 2002-11-20
```

```
; NUMBER OF SEQ ID NOS: 982914
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 135431
```

```
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-135431
```

```
Query Match          74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GTGGAATTATACGACCA 20
        |||||
Db      5 GAGGCATTATACGACCA 22
```

```
RESULT 5
US-10-719-900-265411/C
```

```
; Sequence 265411, Application US/10719900
```

```
; Publication No. US20050026164A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
```

```
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
```

```
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
```

```
; CURRENT FILING DATE: 2003-11-20
```

```
; PRIOR APPLICATION NUMBER: 60/427,808
```

```
; PRIOR FILING DATE: 2002-11-20
```

```
; NUMBER OF SEQ ID NOS: 982914
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 265411
```

```
; LENGTH: 25
```

```
; TYPE: DNA
```

```
; ORGANISM: Mus musculus
```

```
US-10-719-900-265411
```

```
Query Match          74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GTGGAATTATACGACCA 20
        |||||
Db      19 GTGGAATATACGACCA 2
```

```
RESULT 6
US-11-175-859-7489
```

```
; Sequence 7489, Application US/11175859
```

```
; Publication No. US20060024715A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Affymetrix, Inc.
```

```
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
```

```
; FILE REFERENCE: 3690.1
```

```
; CURRENT APPLICATION NUMBER: US/11/175,859
```

```
; CURRENT FILING DATE: 2005-07-05
```

```
; PRIOR APPLICATION NUMBER: US 60/585,352
```

```
; PRIOR FILING DATE: 2004-07-02
```

```
; NUMBER OF SEQ ID NOS: 116251
```

```
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 7489
```

```
; LENGTH: 50
```

```
; TYPE: DNA
```

```
; ORGANISM: homo sapien
```

```
US-11-175-859-7489
```

```
Query Match          74.0%; Score 14.8; DB 16; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 ACGTGAATTATACGACCA 20
        |||||
Db      8 ACATGTATATATACGACGTA 27
```

```
RESULT 7
```

```
US-11-175-859-91821/c
; Sequence 91821, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 91821
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-91821

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 16; Length 50;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTGAATTATACCAAGCC 19
Db 48 CATGAATTATACCAAGCC 31

RESULT 8
US-10-719-900-962131/c
; Sequence 962131, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 962131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-962131

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 9; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGAATTATACCAAGCC 20
Db 20 GGAATGATACCAAGCC 5

RESULT 9
US-10-719-956-169821
; Sequence 169821, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169821
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-169821

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATACCAAGCC 19
Db 6 ACGTGAGTGTACCAAGCC 24

RESULT 10
US-10-719-956-169822
; Sequence 169822, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-169822

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATACCAAGCC 19
Db 6 ACGTGAGTGTACCAAGCC 24

RESULT 11
US-10-719-900-467341
; Sequence 467341, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 467341
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-467341

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 9; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACGTGAATTATACCAAGCC 19
Db 5 ACGTGAGTGTACCAAGCC 23

RESULT 12
```

```
US-10-956-157-15043/c
; Sequence 15043, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15043
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-15043
```

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Query Match      71.0% Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2% Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 CGTGAATTATACAGCCA 20
DB      19 CGTGAAGATTAACAGCCA 1
```

```
RESULT 13
US-10-956-157-15044/c
; Sequence 15044, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15044
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-15044
```

```
Query Match      71.0% Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2% Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 CGTGAATTATACAGCCA 20
DB      20 CGTGAAGATTAACAGCCA 2
```

```
RESULT 14
US-10-956-157-190558/c
; Sequence 190558, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190558
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-190558
```

```
Query Match      71.0% Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2% Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 CGTGAATTATACAGCCA 20
DB      20 CGTGAAGATTAACAGCCA 2
```

```
RESULT 15
US-10-932-182A-135456
; Sequence 135456, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-135456
```

```
Query Match      71.0% Score 14.2; DB 11; Length 25;
Best Local Similarity 84.2% Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 ACGTGAATTATACAGGCC 19
DB      5 ACGTCCGATTATACAGGCC 23
```

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Search completed: May 23, 2006, 11:53:35
Job time : 979 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 11:37:18 ; Search time 50 Seconds
(without alignments)
28.222 Million cell updates/sec

Title: US-10-714-796-122

Perfect score: 20

Sequence: 1 acgtggaattatcacagcca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 393418

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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3: /EMC_Celestra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB_seq.*
4: /EMC_Celestra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB_seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	25	US-11-217-529-135456	Sequence 135456, A
2	13.8	69.0	25	US-11-217-529-115814	Sequence 115814, A
3	13.6	68.0	25	US-11-238-282-11	Sequence 11, Appl
4	13.4	67.0	25	US-11-217-529-184614	Sequence 184614, A
5	13.2	66.0	25	US-11-217-529-55862	Sequence 55862, A
6	12.8	64.0	25	US-11-217-529-45848	Sequence 45848, A
7	12.8	64.0	25	US-11-217-529-61089	Sequence 61089, A
8	12.8	64.0	25	US-11-217-529-92822	Sequence 92822, A
9	12.8	64.0	25	US-11-217-529-103876	Sequence 103876, A
10	12.6	63.0	25	US-11-217-529-6691	Sequence 6691, Ap
11	12.6	63.0	25	US-11-217-529-23381	Sequence 23381, A
12	12.4	62.0	25	US-11-217-529-112299	Sequence 112299, A
13	12.2	61.0	25	US-11-217-529-8938	Sequence 8938, Ap
14	12.2	61.0	25	US-11-217-529-13433	Sequence 13433, A
15	12.2	61.0	25	US-11-217-529-35203	Sequence 35203, A
16	12.2	61.0	25	US-11-217-529-36523	Sequence 36523, A
17	12.2	61.0	25	US-11-217-529-179966	Sequence 179966, A
18	12.2	61.0	25	US-11-217-529-189355	Sequence 189355, A
19	12.2	61.0	25	US-11-217-529-193006	Sequence 193006, A
20	12.2	61.0	25	US-11-217-529-193007	Sequence 193007, A
21	12.2	61.0	25	US-11-217-529-193009	Sequence 193009, A
22	12.2	61.0	25	US-11-217-529-11032	Sequence 11032, A
23	12.2	60.0	25	US-11-217-529-33385	Sequence 33385, A
24	12.2	60.0	25	US-11-217-529-33692	Sequence 33692, A
25	12.2	60.0	25	US-11-217-529-61237	Sequence 61237, A

c	26	12	60.0	25	7	US-11-217-529-93539	Sequence 93539, A
c	27	12	60.0	25	7	US-11-217-529-105215	Sequence 105215, A
c	28	12	60.0	25	7	US-11-217-529-146223	Sequence 146223, A
c	29	12	60.0	25	7	US-11-217-529-169263	Sequence 169263, A
c	30	12	60.0	25	7	US-11-143-642-1422	Sequence 1422, Ap
c	31	11.8	59.0	25	7	US-11-217-529-37938	Sequence 37938, A
c	32	11.8	59.0	25	7	US-11-217-529-92308	Sequence 92308, A
c	33	11.8	59.0	25	7	US-11-217-529-107278	Sequence 107278, A
c	34	11.8	59.0	25	7	US-11-217-529-114640	Sequence 114640, A
c	35	11.8	59.0	25	7	US-11-217-529-122996	Sequence 122996, A
c	36	11.8	59.0	25	7	US-11-217-529-129513	Sequence 129513, A
c	37	11.8	59.0	25	7	US-11-217-529-193004	Sequence 193004, A
c	38	11.8	59.0	25	7	US-11-217-529-54791	Sequence 54791, A
c	39	11.6	58.0	25	7	US-11-217-529-28242	Sequence 28242, A
c	40	11.6	58.0	25	7	US-11-217-529-33205	Sequence 33205, A
c	41	11.6	58.0	25	7	US-11-217-529-34626	Sequence 34626, A
c	42	11.6	58.0	25	7	US-11-217-529-61646	Sequence 61646, A
c	43	11.6	58.0	25	7	US-11-217-529-72067	Sequence 72067, A
c	44	11.6	58.0	25	7	US-11-217-529-72753	Sequence 72753, A
c	45	11.6	58.0	25	7	US-11-217-529-72753	Sequence 72753, A

ALIGNMENTS

RESULT 1
US-11-217-529-135456
; Sequence 135456, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORO LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-135456
Query Match 71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 5 ACGTCCATTATCACGCC 23
1 ACGTGAATTATCACGCC 19
US-11-217-529-115814
; Sequence 115814, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORO LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 115814
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-115814

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACCAAG 17
DB 5 ACGTGAATTATACCAAG 21

RESULT 3
US-11-238-282-11
/ Sequence 11, Application US/11238282
/ Publication No. US20060089303a1
/ GENERAL INFORMATION:
/ APPLICANT: Old, Lloyd J.
/ APPLICANT: Scanlan, Matthew J.
/ APPLICANT: Chen, Yao-Tseng
/ TITLE OF INVENTION: Cancer-Testis Antigens
/ FILE REFERENCE: 10461.70125US01
/ CURRENT APPLICATION NUMBER: US/11/238,282
/ CURRENT FILING DATE: 2005-09-29
/ PRIOR APPLICATION NUMBER: US 10/054,683
/ PRIOR FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: US 60/280,718
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: US 60/285,154
/ PRIOR FILING DATE: 2001-04-20
/ PRIOR APPLICATION NUMBER: US 60/327,432
/ PRIOR FILING DATE: 2001-10-05
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 11
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Probe
US-11-238-282-11

Query Match 68.0%; Score 13.6; DB 7; Length 29;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACCAAG 20
DB 3 ACGTGAATTATACCAAG 22

RESULT 4
US-11-217-529-184614/c
/ Sequence 184614, Application US/11217529
/ Publication No. US20060099612a1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIRO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529

/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 184614
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-184614

Query Match 67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGAATTATACCAAG 18
DB 22 TGAATTATACCAAG 8

RESULT 5
US-11-217-529-55862/c
/ Sequence 55862, Application US/11217529
/ Publication No. US20060099612a1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIRO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 55862
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-55862

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTGAATTATACCAAG 19
DB 19 CTTGAGTTATACCTGCC 2

RESULT 6
US-11-217-529-45848
/ Sequence 45848, Application US/11217529
/ Publication No. US20060099612a1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIRO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3

SEQ ID NO 45848
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-45848

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAATTATACCGCCA 20
DB 1 GGAATTATACCGCCA 16

RESULT 7
US-11-217-529-61089
Sequence 61089, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 61089
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-61089

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAATTATACCGCCA 20
DB 1 GGAATTATACCGCCA 16

RESULT 8
US-11-217-529-92822/C
Sequence 92822, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 92822
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-92822

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAATTATACCGCCA 20
DB 19 GCAATGATATACCGCCA 4

RESULT 9
US-11-217-529-103876
Sequence 103876, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 103876
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-103876

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTGAATTATACCG 17
DB 8 CGCAGATTATACCG 23

RESULT 10
US-11-217-529-6691
Sequence 6691, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6691
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-6691

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Wed May 24 10:03:07 2006

APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 36205
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-36205

Query Match 61.0%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGTGAATTATACCAG 17
|||
Db 24 ACGTGAAGCATCCAG 8

Search completed: May 23, 2006, 11:54:31
Job time : 50 secs

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